

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: OSTERHOFF, CAROLINE  
I'VELL, RICHARD
- (ii) TITLE OF INVENTION: EPIDIDYMEIS-SPECIFIC RECEPTOR PROTEIN
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: NIXON & VANDERHYE P.C.
  - (B) STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
  - (C) CITY: ARLINGTON
  - (D) STATE: VA
  - (E) COUNTRY: USA
  - (F) ZIP: 22201
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DCS/MS-DCS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: SADOFF, B.J.
  - (B) REGISTRATION NUMBER: 36,663
  - (C) REFERENCE/DOCKET NUMBER: 35-125
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 703-816-4000
  - (B) TELEFAX: 703-816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4665 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..3114
- (ix) FEATURE:
  - (A) NAME/KEY: 3'UTR
  - (B) LOCATION: 3115..4665
- (ix) FEATURE:
  - (A) NAME/KEY: polyA-site
  - (B) LOCATION: 4647..4652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGC CAG CCC GAG GAC GCG AGC GGC AGG TGT GCA CAG AGG TTC TCC ACT	48
Ser Gln Pro Glu Asp Ala Ser Gly Arg Cys Ala Gln Arg Phe Ser Thr	
1 5 10 15	
TTG TTT TCT GAA CTC GCG GTC AGG ATG GTT TTC TCT GTC AGG CAG TGT	96
Leu Phe Ser Glu Leu Ala Val Arg Met Val Phe Ser Val Arg Gln Cys	
20 25 30	
GGC CAT GTT GGC AGA ACT GAA GAA GTT TTA CTG ACG TTC AAG ATA TTC	144
Gly His Val Gly Arg Thr Glu Glu Val Leu Leu Thr Phe Lys Ile Phe	
35 40 45	
CTT GTC ATC ATT TGT CTT CAT GTC GTT CTG GTA ACA TCC CTG GAA GAA	192
Leu Val Ile Ile Cys Leu His Val Val Leu Val Thr Ser Leu Glu Glu	
50 55 60	
GAT ACT GAT AAT TCC AGT TTG TCA CCA CCA CCT GCT AAA TTA TCT GTT	240
Asp Thr Asp Asn Ser Ser Leu Ser Pro Pro Pro Ala Lys Leu Ser Val	
65 70 75 80	
GTC AGT TTT GCC CCC TCC TCC AAT GAG GTT GAA ACA ACA AGC CTC AAT	288
Val Ser Phe Ala Pro Ser Ser Asn Glu Val Glu Thr Thr Ser Leu Asn	
85 90 95	
GAT GTT ACT TTA AGC TTA CTC COT TCA AAC GAA ACA GAA AAA ACT AAA	336
Asp Val Thr Leu Ser Leu Leu Pro Ser Asn Glu Thr Glu Lys Thr Lys	
100 105 110	
ATC ACT ATA GTA AAA ACC TTC AAT GCT TCA GGC GTC AAA CCC CAG AGA	384
Ile Thr Ile Val Lys Thr Phe Asn Ala Ser Gly Val Lys Pro Gln Arg	
115 120 125	
AAT ATC TGC AAT TTG TCA TCT AAT TGC AAT GAC TCA GCA TTT TTT AGA	432
Asn Ile Cys Asn Leu Ser Ser Ile Cys Asn Asp Ser Ala Phe Phe Arg	
130 135 140	
GGT GAG ATC ATG TTT CAA TAT GAT AAA GAA AGC ACT GTT CCC CAG AAT	480
Gly Glu Ile Met Phe Gln Tyr Asp Lys Glu Ser Thr Val Pro Gln Asn	
145 150 155 160	
CAA CAT ATA ACG AAT GGC ACC TTA ACT GGA GTC CTG TCT CTA AGT GAA	528
Gln His Ile Thr Asn Gly Thr Leu Thr Gly Val Leu Ser Leu Ser Glu	
165 170 175	
TTA AAA CGC TCA GAG CTC AAC AAA ACC CTG CAA ACC CTA AGT GAG ACT	576
Leu Lys Arg Ser Glu Leu Asn Lys Thr Leu Gln Thr Leu Ser Glu Thr	
180 185 190	
TAC TTT ATA ATG TGT GCT ACA GCA GAG GCC CAA AGC ACA TTA AAT TGT	624
Tyr Phe Ile Met Cys Ala Thr Ala Glu Ala Gln Ser Thr Leu Asn Cys	
195 200 205	
ACA TTC ACA ATA AAA CTG AAT AAT ACA ATG AAT GCA TGT GCT GCA ATA	672
Thr Phe Thr Ile Lys Leu Asn Asn Thr Met Asn Ala Cys Ala Ala Ile	
210 215 220	
GCC GCT TTG GAA AGA GTA AAG ATT CGA CCA ATG GAA CAC TGC TGC TGT	720
Ala Ala Leu Glu Arg Val Lys Ile Arg Pro Met Glu His Cys Cys Cys	

225					230					235					240	
TCT	GTC	AGG	ATA	CCC	TGC	CCT	TCC	TCC	CCA	GAA	GAG	TTG	GGA	AAG	CTT	768
Ser	Val	Arg	Ile	Pro	Cys	Pro	Ser	Ser	Pro	Glu	Glu	Leu	Gly	Lys	Leu	
				245					250					255		
CAG	TGT	GAC	CTG	CAG	GAT	CCC	ATT	GTC	TGT	CTT	GCT	GAC	CAT	CCA	CGT	816
Gln	Cys	Asp	Leu	Gln	Asp	Pro	Ile	Val	Cys	Leu	Ala	Asp	His	Pro	Arg	
			260					265					270			
GGC	CCA	CCA	TTT	TCT	TCC	AGC	CAA	TCC	ATC	CCA	GTG	GTG	CCT	CGG	GCC	864
Gly	Pro	Pro	Phe	Ser	Ser	Ser		Ser	Ile	Pro	Val	Val	Pro	Arg	Ala	
			275				280					285				
ACT	GTG	CTT	TCC	CAG	GTC	CCC	AAA	GCT	ACC	TCT	TTT	GCT	GAG	CCT	CCA	912
Thr	Val	Leu	Ser	Gln	Val	Pro	Lys	Ala	Thr	Ser	Phe	Ala	Glu	Pro	Pro	
	290					295					300					
GAT	TAT	TCA	CCT	GTG	ACC	CAC	AAT	GTT	CCC	TCT	CCA	ATA	GGG	GAG	ATT	960
Asp	Tyr	Ser	Pro	Val	Thr	His	Asn	Val	Pro	Ser	Pro	Ile	Gly	Glu	Ile	
305					310					315					320	
CAA	CCC	CTT	TCA	CCC	CAG	CCT	TCA	GCT	CCC	ATA	GCT	TCC	AGC	CCT	GCC	1008
Gln	Pro	Leu	Ser	Pro	Gln	Pro	Ser	Ala	Pro	Ile	Ala	Ser	Ser	Pro	Ala	
				325					330					335		
ATT	GAC	ATG	CCC	CCA	CAG	TCT	GAA	ACG	ATC	TCT	TCC	CCT	ATG	CCC	CAA	1056
Ile	Asp	Met	Pro	Pro	Gln	Ser	Glu	Thr	Ile	Ser	Ser	Pro	Met	Pro	Gln	
			340					345					350			
ACC	CAT	GTC	TCC	GGC	ACC	CCA	CCT	CCT	GTG	AAA	GCC	TCA	TTT	TCC	TCT	1104
Thr	His	Val	Ser	Gly	Thr	Pro	Pro	Pro	Val	Lys	Ala	Ser	Phe	Ser	Ser	
			355				360					365				
CCC	ACC	GTG	TCT	GCC	CCT	GCG	AAT	GTC	AAC	ACT	ACC	AGC	GCA	CCT	CCT	1152
Pro	Thr	Val	Ser	Ala	Pro	Ala	Asn	Val	Asn	Thr	Thr	Ser	Ala	Pro	Pro	
	370					375					380					
GTC	CAG	ACA	GAC	ATC	GTC	AAC	ACC	AGC	AGT	ATT	TCT	GAT	CTT	GAG	AAC	1200
Val	Gln	Thr	Asp	Ile	Val	Asn	Thr	Ser	Ser	Ile	Ser	Asp	Leu	Glu	Asn	
385					390					395					400	
CAA	GTG	TTG	CAG	ATG	GAG	AAG	GCT	CTG	TCC	TTG	GGC	AGC	CTG	GAG	CCT	1248
Gln	Val	Leu	Gln	Met	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Ser	Leu	Glu	Pro	
				405				410					415			
AAC	CTC	GCA	GGA	GAA	ATG	ATC	AAC	CAA	GTC	AGC	AGA	CTC	CTT	CAT	TCC	1296
Asn	Leu	Ala	Gly	Glu	Met	Ile	Asn	Gln	Val	Ser	Arg	Leu	Leu	His	Ser	
			420					425					430			
CCG	CCT	GAC	ATG	CTG	GCC	CCT	CTG	GCT	CAA	AGA	TTG	CTG	AAA	GTA	GTG	1344
Pro	Pro	Asp	Met	Leu	Ala	Pro	Leu	Ala	Gln	Arg	Leu	Leu	Lys	Val	Val	
			435				440					445				
GAT	GAC	ATT	GGC	CTA	CAG	CTG	AAC	TTT	TCA	AAC	ACG	ACT	ATA	AGT	CTA	1392
Asp	Asp	Ile	Gly	Leu	Gln	Leu	Asn	Phe	Ser	Asn	Thr	Thr	Ile	Ser	Leu	
	450					455					460					
ACC	TCC	CCT	TCT	TTG	GCT	CTG	GCT	GTG	ATC	AGA	GTG	AAT	GCC	AGT	AGT	1440
Thr	Ser	Pro	Ser	Leu	Ala	Leu	Ala	Val	Ile	Arg	Val	Asn	Ala	Ser	Ser	
	465				470					475					480	

TTC	AAC	ACA	ACT	ACC	TTT	GTG	GCC	CAA	GAC	CCT	GCA	AAT	CTT	CAG	GTT	1488
Phe	Asn	Thr	Thr	Thr	Phe	Val	Ala	Gln	Asp	Pro	Ala	Asn	Leu	Gln	Val	
				485					490					495		
TCT	CTG	GAA	ACC	CAA	GCT	CCT	GAG	AAC	AGT	ATT	GGC	ACA	ATT	ACT	CTT	1536
Ser	Leu	Glu	Thr	Gln	Ala	Pro	Glu	Asn	Ser	Ile	Gly	Thr	Ile	Thr	Leu	
			500					505					510			
CCT	TCA	TCG	CTG	ATG	AAT	AAT	TTA	CCA	GCT	CAT	GAC	ATG	GAG	CTA	GCT	1584
Pro	Ser	Ser	Leu	Met	Asn	Asn	Leu	Pro	Ala	His	Asp	Met	Glu	Leu	Ala	
		515					520					525				
TCC	AGG	GTT	CAG	TTC	AAT	TTT	TTT	GAA	ACA	CCT	GCT	TTG	TTT	CAG	GAT	1632
Ser	Arg	Val	Gln	Phe	Asn	Phe	Phe	Glu	Thr	Pro	Ala	Leu	Phe	Gln	Asp	
	530					535					540					
CCT	TCC	CTG	GAG	AAC	CTC	TCT	CTG	ATC	AGC	TAC	GTC	ATA	TCA	TCG	AGT	1680
Pro	Ser	Leu	Glu	Asn	Leu	Ser	Leu	Ile	Ser	Tyr	Val	Ile	Ser	Ser	Ser	
545					550					555					560	
GTT	GCA	AAC	CTG	ACC	GTC	AGG	AAC	TTG	ACA	AGA	AAC	GTG	ACA	GTC	ACA	1728
Val	Ala	Asn	Leu	Thr	Val	Arg	Asn	Leu	Thr	Arg	Asn	Val	Thr	Val	Thr	
				565					570					575		
TTA	AAG	CAC	ATC	AAC	CCG	AGC	CAG	GAT	GAG	TTA	ACA	GTG	AGA	TGT	GTA	1776
Leu	Lys	His	Ile	Asn	Pro	Ser	Gln	Asp	Glu	Leu	Thr	Val	Arg	Cys	Val	
			580					585					590			
TTT	TGG	GAC	TTG	GGC	AGA	AAT	GGT	GGC	AGA	GGA	GGC	TGG	TCA	GAC	AAT	1824
Phe	Trp	Asp	Leu	Gly	Arg	Asn	Gly	Gly	Arg	Gly	Gly	Trp	Ser	Asp	Asn	
		595					600					605				
GGC	TGC	TCT	GTC	AAA	GAC	AGG	AGA	TTG	AAT	GAA	ACC	ATC	TGT	ACC	TGT	1872
Gly	Cys	Ser	Val	Lys	Asp	Arg	Arg	Leu	Asn	Glu	Thr	Ile	Cys	Thr	Cys	
	610					615					620					
AGC	CAT	CTA	ACA	AGC	TTC	GGC	GTT	CTG	CTG	GAC	CTA	TCT	AGG	ACA	TCT	1920
Ser	His	Leu	Thr	Ser	Phe	Gly	Val	Leu	Leu	Asp	Leu	Ser	Arg	Thr	Ser	
625					630					635					640	
GTG	CTG	CCT	GCT	CAA	ATG	ATG	GCT	CTG	ACG	TTC	ATT	ACA	TAT	ATT	GGT	1968
Val	Leu	Pro	Ala	Gln	Met	Met	Ala	Leu	Thr	Phe	Ile	Thr	Tyr	Ile	Gly	
				645					650					655		
TGT	GGG	CTT	TCA	TCA	ATT	TTT	CTG	TCA	GTG	ACT	CTT	GTA	ACC	TAC	ATA	2016
Cys	Gly	Leu	Ser	Ser	Ile	Phe	Leu	Ser	Val	Thr	Leu	Val	Thr	Tyr	Ile	
			660					665					670			
GCT	TTT	GAA	AAG	ATC	CGG	AGG	GAT	TAC	CCT	TCC	AAA	ATC	CTC	ATC	CAG	2064
Ala	Phe	Glu	Lys	Ile	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu	Ile	Gln	
		675					680					685				
CTG	TGT	GCT	GCT	CTG	CTT	CTG	CTG	AAC	CTG	GTC	TTC	CTC	CTG	GAC	TCG	2112
Leu	Cys	Ala	Ala	Leu	Leu	Leu	Leu	Asn	Leu	Val	Phe	Leu	Leu	Asp	Ser	
		690					695				700					
TGG	ATT	GCT	CTG	TAT	AAG	ATG	CAA	GGC	CTC	TGC	ATC	TCA	GTG	GCT	GTA	2160
Trp	Ile	Ala	Leu	Tyr	Lys	Met	Gln	Gly	Leu	Cys	Ile	Ser	Val	Ala	Val	
705					710					715					720	
TTT	CTT	CAT	TAT	TTT	CTC	TTG	GTC	TCA	TTC	ACA	TGG	ATG	GGC	CTA	GAA	2208
Phe	Leu	His	Tyr	Phe	Leu	Leu	Val	Ser	Phe	Thr	Trp	Met	Gly	Leu	Glu	



AAT GGA AAT GCT TCT ACA GAG AGG AAT GGG GTC TCT TTT AGT GTT CAG Asn Gly Asn Ala Ser Thr Glu Arg Asn Gly Val Ser Phe Ser Val Gln 980 985 990	2976
AAT GGA GAT GTG TGC CTT CAC GAT TTC ACT GGA AAA CAG CAC ATG TTT Asn Gly Asp Val Cys Leu His Asp Phe Thr Gly Lys Gln His Met Phe 995 1000 1005	3024
AAC GAG AAG GAA GAT TCC TGC AAT GGG AAA GGC CGT ATG GCT CTC AGA Asn Glu Lys Glu Asp Ser Cys Asn Gly Lys Gly Arg Met Ala Leu Arg 1010 1015 1020	3072
AGG ACT TCA AAG CGG GGA AGC TTA CAC TTT ATT GAG CAA ATG Arg Thr Ser Lys Arg Gly Ser Leu His Phe Ile Glu Gln Met 1025 1030 1035	3114
TGATTCCTTT CTTCTAAAT CAAAGCATGA TGCTTGACAG TGTGAAATGT CCAATTTTAC	3174
CTTTTACACA ATGTGAGATG TATGAAATC AACTCATTTT ATTCTCGGCA ACATCTGGAG	3234
AAGCATAAGC TAATTAAGGG CGATGATTAT TATTACAGA AGAAACCAAG ACATTACACC	3294
ATGGTTTTTA GACATTTCTG ATTTGGTTTC TATCTTTCA TTTTATAAGA AGGTTGGTTT	3354
TAAACAATAC ACTAAGAATG ACTCCTATAA AGAAACAAA AAAAGGTAGT GAACCTTCAG	3414
CTACCTTTTA AAGAGGCTAA GTTATCTTTG ATAACATCAT ATAAAGCAAC TGTTGACTTC	3474
AGCCTGTTGG TGAGTTTAGT TGTGCATGCC TTTGTTGTAT ATAGCTTAA TTCTAGTGAC	3534
CCATGTGTCA AAAATCTTAC TTCTACATTT TTTTGTATTT ATTTTCTACT GTGTAAATGT	3594
ATTCCTTTGT AGAATCATGG TTGTTTTGTC TCACGTGATA ATTCAGAAAA TCCTTGCTCG	3654
TTCCGCAAT CCTAAAGCTC CTTTTGGAGA TGATATAGGA TGTGAAATAC AGAAACCTCA	3714
GTGAAATCAA GAAATAATGA TCCCAGCCAG ACTGAGAAAA TGTAAGCAGA CAGTGCCACA	3774
GTTAGCTCAT ACAGTGCCTT TGAGCAAGTT AGGAAAAGAT GCCCCCACTG GGCAGACACA	3834
GCCCTATGGG TCATGGTTTG ACAAACAGAG TGAGAGACCA TATTTTAGCC CCACTCACCC	3894
TCTTNGGTGC ACGACCTGTA CAGCCAAACA CAGCTCCCA TATGAATACC CATCCCCTGA	3954
CCGCATCCCC AGTAGTCAGA TTATAGAATC TGCACCAAGA TGTTTAGCTT TATACCTTGG	4014
CCACAGAGAG GGATGAACTG TCATCCAGAC CATGTGTGAG GAAAATTGTG AACGTAGATG	4074
AGGTACATAC ACTGCCGCTT CTCAATCCC CAGAGCCTTT AGGAACAGGA GAGTAGACTA	4134
GGATTCCTTC TCTTAAAAAG GTACATATAT ATGGAAAAAA ATCATATTGC CGTTCCTTAA	4194
AAGGCAACTG CATGGTACAT TGTGTATTGT TATGACTGGT ACACTCTGGC CCAGCCAGAG	4254
CTATAATTGT TTTTAAATG TGTCTTGAAG AATGCACAGT GANAAGGGGA GTAGCTATTG	4314
GGAACAGGGA ACTGTCCTAC ACTGCTATTG TTGCTACATG TATCGAGCCT TGATTGCTCC	4374
TAGTTATATA CAGGGTCTAT CTTGCTTCCT ACCTACATCT GCTTGAGCAG TGCTCAAGT	4434
ACATCCTTAT TAGGAACATT TCAAACCCCT TTTAGTTAAG TCTTTCACCTA AGGTTCTCTT	4494

GCATATATTT CAAGTGAATG TTGGATCTCA GACTAACCAT AGTAATAATA CACATTTCTG 4554  
 TGAGTGCTGA CTTGTCTTTG CAATATTTCT TTTCTGATTT ATTTAATTTT CTTGTATTTA 4614  
 TATGTTAAAA TCAAAAATGT TAAAATCAAT GAAATAAATT TGCAGTTAAG A 4665

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ser	Gln	Pro	Glu	Asp	Ala	Ser	Gly	Arg	Cys	Ala	Gln	Arg	Phe	Ser	Thr	1	5	10	15
Leu	Phe	Ser	Glu	Leu	Ala	Val	Arg	Met	Val	Phe	Ser	Val	Arg	Gln	Cys	20	25	30	
Gly	His	Val	Gly	Arg	Thr	Glu	Glu	Val	Leu	Leu	Thr	Phe	Lys	Ile	Phe	35	40	45	
Leu	Val	Ile	Ile	Cys	Leu	His	Val	Val	Leu	Val	Thr	Ser	Leu	Glu	Glu	50	55	60	
Asp	Thr	Asp	Asn	Ser	Ser	Leu	Ser	Pro	Pro	Pro	Ala	Lys	Leu	Ser	Val	65	70	75	80
Val	Ser	Phe	Ala	Pro	Ser	Ser	Asn	Glu	Val	Glu	Thr	Thr	Ser	Leu	Asn	85	90	95	
Asp	Val	Thr	Leu	Ser	Leu	Leu	Pro	Ser	Asn	Glu	Thr	Glu	Lys	Thr	Lys	100	105	110	
Ile	Thr	Ile	Val	Lys	Thr	Phe	Asn	Ala	Ser	Gly	Val	Lys	Pro	Gln	Arg	115	120	125	
Asn	Ile	Cys	Asn	Leu	Ser	Ser	Ile	Cys	Asn	Asp	Ser	Ala	Phe	Phe	Arg	130	135	140	
Gly	Glu	Ile	Met	Phe	Gln	Tyr	Asp	Lys	Glu	Ser	Thr	Val	Pro	Gln	Asn	145	150	155	160
Gln	His	Ile	Thr	Asn	Gly	Thr	Leu	Thr	Gly	Val	Leu	Ser	Leu	Ser	Glu	165	170	175	
Leu	Lys	Arg	Ser	Glu	Leu	Asn	Lys	Thr	Leu	Gln	Thr	Leu	Ser	Glu	Thr	180	185	190	
Tyr	Phe	Ile	Met	Cys	Ala	Thr	Ala	Glu	Ala	Gln	Ser	Thr	Leu	Asn	Cys	195	200	205	
Thr	Phe	Thr	Ile	Lys	Leu	Asn	Asn	Thr	Met	Asn	Ala	Cys	Ala	Ala	Ile	210	215	220	

Ala	Ala	Leu	Glu	Arg	Val	Lys	Ile	Arg	Pro	Met	Glu	His	Cys	Cys	Cys	225	230	235	240
Ser	Val	Arg	Ile	Pro	Cys	Pro	Ser	Ser	Pro	Glu	Glu	Leu	Gly	Lys	Leu	245	250	255	
Gln	Cys	Asp	Leu	Gln	Asp	Pro	Ile	Val	Cys	Leu	Ala	Asp	His	Pro	Arg	260	265	270	
Gly	Pro	Pro	Phe	Ser	Ser	Ser	Gln	Ser	Ile	Pro	Val	Val	Pro	Arg	Ala	275	280	285	
Thr	Val	Leu	Ser	Gln	Val	Pro	Lys	Ala	Thr	Ser	Phe	Ala	Glu	Pro	Pro	290	295	300	
Asp	Tyr	Ser	Pro	Val	Thr	His	Asn	Val	Pro	Ser	Pro	Ile	Gly	Glu	Ile	305	310	315	320
Gln	Pro	Leu	Ser	Pro	Gln	Pro	Ser	Ala	Pro	Ile	Ala	Ser	Ser	Pro	Ala	325	330	335	
Ile	Asp	Met	Pro	Pro	Gln	Ser	Glu	Thr	Ile	Ser	Ser	Pro	Met	Pro	Gln	340	345	350	
Thr	His	Val	Ser	Gly	Thr	Pro	Pro	Pro	Val	Lys	Ala	Ser	Phe	Ser	Ser	355	360	365	
Pro	Thr	Val	Ser	Ala	Pro	Ala	Asn	Val	Asn	Thr	Thr	Ser	Ala	Pro	Pro	370	375	380	
Val	Gln	Thr	Asp	Ile	Val	Asn	Thr	Ser	Ser	Ile	Ser	Asp	Leu	Glu	Asn	385	390	395	400
Gln	Val	Leu	Gln	Met	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Ser	Leu	Glu	Pro	405	410	415	
Asn	Leu	Ala	Gly	Glu	Met	Ile	Asn	Gln	Val	Ser	Arg	Leu	Leu	His	Ser	420	425	430	
Pro	Pro	Asp	Met	Leu	Ala	Pro	Leu	Ala	Gln	Arg	Leu	Leu	Lys	Val	Val	435	440	445	
Asp	Asp	Ile	Gly	Leu	Gln	Leu	Asn	Phe	Ser	Asn	Thr	Thr	Ile	Ser	Leu	450	455	460	
Thr	Ser	Pro	Ser	Leu	Ala	Leu	Ala	Val	Ile	Arg	Val	Asn	Ala	Ser	Ser	465	470	475	480
Phe	Asn	Thr	Thr	Thr	Phe	Val	Ala	Gln	Asp	Pro	Ala	Asn	Leu	Gln	Val	485	490	495	
Ser	Leu	Glu	Thr	Gln	Ala	Pro	Glu	Asn	Ser	Ile	Gly	Thr	Ile	Thr	Leu	500	505	510	
Pro	Ser	Ser	Leu	Met	Asn	Asn	Leu	Pro	Ala	His	Asp	Met	Glu	Leu	Ala	515	520	525	
Ser	Arg	Val	Gln	Phe	Asn	Phe	Phe	Glu	Thr	Pro	Ala	Leu	Phe	Gln	Asp	530	535	540	
Pro	Ser	Leu	Glu	Asn	Leu	Ser	Leu	Ile	Ser	Tyr	Val	Ile	Ser	Ser	Ser	545	550	555	560



Val	Ala	Asn	Leu	Thr	Val	Arg	Asn	Leu	Thr	Arg	Asn	Val	Thr	Val	Thr		
				565					570					575			
Leu	Lys	His	Ile	Asn	Pro	Ser	Gln	Asp	Glu	Leu	Thr	Val	Arg	Cys	Val		
			580					585					590				
Phe	Trp	Asp	Leu	Gly	Arg	Asn	Gly	Gly	Arg	Gly	Gly	Trp	Ser	Asp	Asn		
		595					600					605					
Gly	Cys	Ser	Val	Lys	Asp	Arg	Arg	Leu	Asn	Glu	Thr	Ile	Cys	Thr	Cys		
	610					615					620						
Ser	His	Leu	Thr	Ser	Phe	Gly	Val	Leu	Leu	Asp	Leu	Ser	Arg	Thr	Ser		
625					630					635					640		
Val	Leu	Pro	Ala	Gln	Met	Met	Ala	Leu	Thr	Phe	Ile	Thr	Tyr	Ile	Gly		
				645					650					655			
Cys	Gly	Leu	Ser	Ser	Ile	Phe	Leu	Ser	Val	Thr	Leu	Val	Thr	Tyr	Ile		
			660					665					670				
Ala	Phe	Glu	Lys	Ile	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu	Ile	Gln		
		675					680					685					
Leu	Cys	Ala	Ala	Leu	Leu	Leu	Leu	Asn	Leu	Val	Phe	Leu	Leu	Asp	Ser		
	690					695					700						
Trp	Ile	Ala	Leu	Tyr	Lys	Met	Gln	Gly	Leu	Cys	Ile	Ser	Val	Ala	Val		
705					710					715					720		
Phe	Leu	His	Tyr	Phe	Leu	Leu	Val	Ser	Phe	Thr	Trp	Met	Gly	Leu	Glu		
				725					730					735			
Ala	Phe	His	Met	Tyr	Leu	Ala	Leu	Val	Lys	Val	Phe	Asn	Thr	Tyr	Ile		
			740				745						750				
Arg	Lys	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Val	Gly	Trp	Gly	Val	Pro	Ala		
		755					760					765					
Val	Val	Val	Thr	Ile	Ile	Leu	Thr	Ile	Ser	Pro	Asp	Asn	Tyr	Gly	Leu		
	770					775					780						
Gly	Ser	Tyr	Gly	Lys	Phe	Pro	Asn	Gly	Ser	Pro	Asp	Asp	Phe	Cys	Trp		
785					790				795					800			
Ile	Asn	Asn	Asn	Ala	Val	Phe	Tyr	Ile	Thr	Val	Val	Gly	Tyr	Phe	Cys		
				805					810					815			
Val	Ile	Phe	Leu	Leu	Asn	Val	Ser	Met	Phe	Ile	Val	Val	Leu	Val	Gln		
			820					825					830				
Leu	Cys	Arg	Ile	Lys	Lys	Lys	Lys	Gln	Leu	Gly	Ala	Gln	Arg	Lys	Thr		
		835					840					845					
Ser	Ile	Gln	Asp	Leu	Arg	Ser	Ile	Ala	Gly	Leu	Thr	Phe	Leu	Leu	Gly		
	850					855					860						
Ile	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Val	Asn	Val	Thr		
865					870					875				880			
Phe	Met	Tyr	Leu	Phe	Ala	Ile	Phe	Asn	Thr	Leu	Gln	Gly	Phe	Phe	Ile		

885										890					895				
Phe	Ile	Phe	Tyr	Cys	Val	Ala	Lys	Glu	Asn	Val	Arg	Lys	Gln	Trp	Arg				
			900					905					910						
Arg	Tyr	Leu	Cys	Cys	Gly	Lys	Leu	Arg	Leu	Ala	Glu	Asn	Ser	Asp	Trp				
		915					920					925							
Ser	Lys	Thr	Ala	Thr	Asn	Gly	Leu	Lys	Lys	Gln	Thr	Val	Asn	Gln	Gly				
	930					935					940								
Val	Ser	Ser	Ser	Ser	Asn	Ser	Leu	Gln	Ser	Ser	Ser	Asn	Ser	Thr	Asn				
	945				950				955						960				
Ser	Thr	Thr	Leu	Leu	Val	Asn	Asn	Asp	Cys	Ser	Val	His	Ala	Ser	Gly				
				965					970						975				
Asn	Gly	Asn	Ala	Ser	Thr	Glu	Arg	Asn	Gly	Val	Ser	Phe	Ser	Val	Gln				
			980					985							990				
Asn	Gly	Asp	Val	Cys	Leu	His	Asp	Phe	Thr	Gly	Lys	Gln	His	Met	Phe				
		995					1000					1005							
Asn	Glu	Lys	Glu	Asp	Ser	Cys	Asn	Gly	Lys	Gly	Arg	Met	Ala	Leu	Arg				
	1010					1015					1020								
Arg	Thr	Ser	Lys	Arg	Gly	Ser	Leu	His	Phe	Ile	Glu	Gln	Met						
	1025				1030					1035									

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala	Phe	Phe	Arg	Gly	Glu	Ile	Met	Phe	Gln	Tyr	Asp	Lys	Glu
1				5					10				

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Leu Ala Asp His Pro Arg Gly Pro Pro Phe Ser Ser Ser Gln  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gly Ser Tyr Gly Lys Phe Pro Asn Gly Ser Pro Asp Asp Phe Cys  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Cys Trp Ile Asn Asn Asn Ala Val Phe Tyr  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Cys Arg Ile Lys Lys Lys Lys Gln Leu Gly Ala Gln Arg Lys Thr  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCTATGGGA GCTGAAG

17

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGTCAATGGC AGGGCTG

17

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATCCGAAAA TACATCC

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGAAGGCACA CATCTCC

17